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continued

	-concinaea
(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:	28:
ATTCAAAGGG TATCTGGGCT CTGG	24
(2) INFORMATION FOR SEQ ID NO: 29:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:	29:
ACTGGCACAG AACAGGCACT TAGG	24
(2) INFORMATION FOR SEQ ID NO: 30:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:	30:
GGAGGAACTG GGAACCACAC AGGT	24
(2) INFORMATION FOR SEQ ID NO: 31:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 29 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:	31:
GAAAGCCCTA GTGGATGATA AGAATAATC	29
(2) INFORMATION FOR SEQ ID NO: 32:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:	32:
GGACAGATGA TAAATACATA GGATGGATGG	30
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What is claimed is:

1. A method of simultaneously determining the alleles present in at least three short tandem repeat loci from one or more DNA samples, comprising:

- a) obtaining at least one DNA sample to be analyzed;
- b) selecting a set of at least three short tandem repeat loci of the DNA sample to be analyzed which can be

co-amplified, wherein the at least three short tandem repeat loci in the set comprises at least three loci selected from the group consisting of:

HUMPOX, HUMTH01 and HUMCD4; HUMTPOX, HUMTH01 and HUMVWFA31; HUMHPRTB, HUMFESFPS and HUMVWFA31;